

Supplemental Table S1. Quantitative evaluation of the deviation from the consensus sequences derived from the protein alignment in Supplemental Figure S2.

	locus identifier	label for encoded protein	number of deviations from general CDA consensus ¹	number of deviations from plant CDA consensus ¹	number of insertions or deletions	Is this protein a functional CDA?
<i>Arabidopsis thaliana</i>	At2g19570	Ath	0	0	0	yes, experimentally confirmed
	At4g29570	Ath-L1	3	19	3	unlikely
	At4g29580.1	Ath-L2	6	24	5	unlikely
	At4g29600	Ath-L3	2	9	2	no, experimentally confirmed
	At4g29610	Ath-L4	1	11	3	no, experimentally confirmed, however deoxycytosine is a substrate processed with very low catalytic efficiency
	At4g29620	Ath-L5	4	13	3	unlikely
	At4g29630	Ath-L6	5	20	3	no, very large deletion
	At4g29640	Ath-L7	9	14	4	unlikely
	At4g29650	Ath-L8	12	19	4	no, very large deletion
<i>Arabidopsis lyrata</i>	480515	Aly	0	0	0	yes
	920886	Aly-L1	2	20	3	unlikely
	328753	Aly-L2	7	19	4	unlikely
	491800	Aly-L3	4	15	2	unlikely
	913535	Aly-L4	1	11	2	unsure
	491799	Aly-L5	2	14	3	unlikely
	491798	Aly-L6	12	24	4	no, very large deletion
	913538	Aly-L7	8	12	4	unlikely
<i>Capsella rubella</i>	Carubv10014260m	Cru	0	1 ²	0	yes
	Carubv10006462m	Cru-L1	1	13	3	unsure
	Carubv10007499m	Cru-L2	6	14	2	unlikely
	Carubv10007223m	Cru-L3	9	19	6	unlikely

¹ see Figure S1 for the deduction of the consensus

² This exchange (A to S at position 98 in Cru) is also observed in Mes1 and Bra2 (see Supplemental Figure S1). Cru is likely to be functional because it is the only well conserved CDA in *Capsella rubella*